

w/ #6A

-1-

SEQUENCE LISTING

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A22



<110> Hanke, Paul D.

Li-D'Elia, Lhing-Yew

Rayapati, John

Crafton, Corey

Walsh, Holly

<120> Increased Lysine Production by Gene Amplification

<130> 1533.1030002

<140> 09/722,441

<141> 2000-11-28

<150> US 60/173,707

<151> 1999-12-30

<150> US 60/184,130

<151> 2000-02-22

<160> 37

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

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gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct 96  
 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
 20 25 30

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144  
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
 35 40 45

gaa ctt cta gaa ctt gca cgc gca gtg aat ccc gtt ccg cca gct cgt 192  
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
 50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240  
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
 65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act 288  
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
 85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336  
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
 100 105 110

att gtt gac gtc aca ccg ggt cgt gtg cgt gaa gca ctc gat gag ggc 384  
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
 115 120 125

aag atc tgc att gtt gct ggt ttt cag ggt gtt aat aaa gaa acc cgc 432  
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
 130 135 140

gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt cgc 480  
 Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala  
 145 150 155 160

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528  
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
 165 170 175

gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag 576  
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
 180 185 190

ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc 624  
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
 195 200 205

tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat 672  
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220

gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg 720  
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240

att gcc ggc tct atg gag gat att cct gtg gaa gca gtc ctt acc 768  
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr

	245	250	255	
ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att				816
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile	260	265	270	
tcc gat aag cca ggc gag gct gcc aag gtt ttc cgt gcg ttg gct gat				864
Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp	275	280	285	
gca gaa atc aac att gac atg gtt ctg cag aac gtc tcc tct gtg gaa				912
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu	290	295	300	
gac ggc acc acc gac atc acg ttc acc tgc cct cgc gct gac gga cgc				960
Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg	305	310	315	320
cgt gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc				1008
Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr	325	330	335	
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct				1056
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala	340	345	350	
ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg				1104
Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu	355	360	365	
cgc gat gtc aac gtg aac atc gaa ttg att tcc atc tct gag atc cgc				1152
Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg	370	375	380	
att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca				1200
Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala	385	390	395	400
ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat				1248
Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr	405	410	415	
gca ggc acc gga cgc taa				1266
Ala Gly Thr Gly Arg	420			
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35 40 45

Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Val Gly  
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg  
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg  
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
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Ala Gly Thr Gly Arg  
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<210> 3

<211> 1035

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1035)

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Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val

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atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt Met Arg Thr Phe Leu Glu Glu Arg Asn 25 Phe Pro Ala Asp Thr Val Arg	20	25	30	96
ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Phe Arg Gly	35	40	45	144
acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu	50	55	60	192
aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Thr Ala Ser Lys	65	70	75	240
cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn	85	90	95	288
tct tct gct tgg cgc aag gac gac gag gtt cca cta atc gtc tct gag Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu	100	105	110	336
gtg aac cct tcc gac aag gat tcc ctg gtc aag ggc att att gcg aat Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn	115	120	125	384
cct aac tgc acc acc atg gct gca atg cca gtg ctg aag cca ctg cac Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His	130	135	140	432
gat gcc gct ggt ctt gta aag ctt cac gtt tcc tct tac cag gct gtt Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val	145	150	155	480
tcc ggt tct ggt ctt gca ggt gtg gaa acc ttg gca aag cag gtt gct Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala	165	170	175	528
gca gtt ggc gac cac aac gtt gag ttc gtc cat gat gga cag gct gct Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala	180	185	190	576
gac gca ggc gat gtc gga cct tac gtt tcc cca atc gct tac aac gtg Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val	195	200	205	624
ctg cca ttc gcc gga aac ctc gtc gat gac ggc acc ttc gaa acc gac Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp	210	215	220	672
gaa gag cag aag ctg cgc aac gaa tcc cgc aag att ctc ggc ctc cca Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro	225	230	235	720
gac ctc aag gtc tca ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly	245	250	255	768

cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag 816  
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu  
260 265 270

cag gcg cag gag atc ttg ggt gcc gct tca ggc gtc gag ctt gtc gac 864  
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp  
275 280 285

gtc cca acc cca ctt gca gct gcc ggc att gac gaa tcc ctc gtt gga 912  
Val Pro Thr Pro Leu Ala Ala Gly Ile Asp Glu Ser Leu Val Gly  
290 295 300

cgc atc cgt cag gac tcc act gtc gac gac aac cgc ggt ctg gtt ctc 960  
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu  
305 310 315 320

gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc att 1008  
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile  
325 330 335

cag att gct gag ctg ctg gtt aag taa 1035  
Gln Ile Ala Glu Leu Leu Val Lys  
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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

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20 25 30

Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
50 55 60

Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu

100		105		110
Val Asn Pro Ser Asp Lys Asp	Ser Leu Val Lys Gly Ile Ile Ala Asn			
115	120	125		
Pro Asn Cys Thr Thr Met Ala	Ala Met Pro Val Leu Lys Pro Leu His			
130	135	140		
Asp Ala Ala Gly Leu Val Lys Leu His Val	Ser Ser Tyr Gln Ala Val			
145	150	155		160
Ser Gly Ser Gly Leu Ala Gly Val Glu Thr	Leu Ala Lys Gln Val Ala			
	165	170		175
Ala Val Gly Asp His Asn Val Glu Phe Val	His Asp Gly Gln Ala Ala			
	180	185		190
Asp Ala Gly Asp Val Gly Pro Tyr Val Ser	Pro Ile Ala Tyr Asn Val			
	195	200		205
Leu Pro Phe Ala Gly Asn Leu Val Asp Asp	Gly Thr Phe Glu Thr Asp			
	210	215		220
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg	Lys Ile Leu Gly Leu Pro			
225	230	235		240
Asp Leu Lys Val Ser Gly Thr Cys Val Arg	Val Pro Val Phe Thr Gly			
	245	250		255
His Thr Leu Thr Ile His Ala Glu Phe Asp	Lys Ala Ile Thr Val Glu			
	260	265		270
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser	Gly Val Glu Leu Val Asp			
	275	280		285
Val Pro Thr Pro Leu Ala Ala Ala Gly Ile	Asp Glu Ser Leu Val Gly			
	290	295		300
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp	Asn Arg Gly Leu Val Leu			
305	310	315		320
Val Val Ser Gly Asp Asn Leu Arg Lys Gly	Ala Ala Leu Asn Thr Ile			
	325	330		335
Gln Ile Ala Glu Leu Leu Val Lys				
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<211> 906

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(906)

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ggt gga gta gca atg gtt act cca ttc acg gaa tcc gga gac atc gat	96	
Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp		
20 25 30		
atc gct gct ggc cgc gaa gtc gcg gct tat ttg gtt gat aag ggc ttg	144	
Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu		
35 40 45		
gat tct ttg gtt ctc gcg ggc acc act ggt gaa tcc cca acg aca acc	192	
Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr		
50 55 60		
gcc gct gaa aaa cta gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg	240	
Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly		
65 70 75 80		
gat cgg gcg aag ctc atc gcc ggt gtc gga acc aac aac acg cgg aca	288	
Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr		
85 90 95		
tct gtg gaa ctt gcg gaa gct gct gct tct gct ggc gca gac ggc ctt	336	
Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly Leu		
100 105 110		
tta gtt gta act cct tat tac tcc aag cgg agc caa gag gga ttg ctg	384	
Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu		
115 120 125		
gcg cac ttc ggt gca att gct gca gca aca gag gtt cca att tgt ctc	432	
Ala His Phe Gly Ala Ile Ala Ala Thr Glu Val Pro Ile Cys Leu		
130 135 140		
tat gac att cct ggt cgg tca ggt att cca att gaa tct gat acc atg	480	
Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met		
145 150 155 160		
aga cgc ctg agt gaa tta cct acg att ttg gcg gtc aag gac gcc aag	528	
Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys		
165 170 175		

ggt gac ctc gtt gca gcc acg tca ttg atc aaa gaa acg gga ctt gcc 576  
 Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala  
 180 185 190

tgg tat tca ggc gat gac cca cta aac ctt gtt tgg ctt gct ttg ggc 624  
 Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly  
 195 200 205

gga tca ggt ttc att tcc gta att gga cat gca gcc ccc aca gca tta 672  
 Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu  
 210 215 220

cgt gag ttg tac aca agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg 720  
 Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg  
 225 230 235 240

gaa atc aac gcc aaa cta tca ccg ctg gta gct gcc caa ggt cgc ttg 768  
 Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu  
 245 250 255

ggt gga gtc agc ttg gca aaa gct gct ctg cgt ctg cag ggc atc aac 816  
 Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn  
 260 265 270

gta gga gat cct cga ctt cca att atg gct cca aat gag cag gaa ctt 864  
 Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu  
 275 280 285

gag gct ctc cga gaa gac atg aaa aaa gct gga gtt cta taa 906  
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<210> 6

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

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 20 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu  
 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr  
 50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly  
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr  
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu  
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu  
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu  
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met  
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys  
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala  
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly  
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu  
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg  
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu  
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn  
260 265 270

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Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  
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<211> 747

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(747)

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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala	
20 25 30	
gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac aac ggc gct	144
Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala	
35 40 45	
gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg ggc aac ctg	192
Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu	
50 55 60	
gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga acc acg ggc	240
Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Gly Thr Thr Gly	
65 70 75 80	
ttc gat aat gct cgt ttg gag cag gtt cgc gcc tgg ctt gaa gga aaa	288
Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys	
85 90 95	
gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc tct gcg gtg	336
Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val	
100 105 110	
ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc gaa tca gct	384
Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala	
115 120 125	
gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca cct tca ggc	432
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly	
130 135 140	
acc gcg atc cac act gct cag ggc att gct gcg gca cgc aaa gaa gca	480
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala	
145 150 155 160	
ggc atg gac gca cag cca gat gcg acc gag cag gca ctt gag ggt tcc	528
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser	
165 170 175	
cgt ggc gca agc gta gat gga atc cca gtt cac gca gtc cgc atg tcc	576
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser	
180 185 190	

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ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag ggt cag acc      624
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
195                200                205

ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt gca cca ggt      672
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
210                215                220

gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc cta gtc gta      720
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
225                230                235                240

gga ctt gag cat tac cta ggc ctg taa      747
Gly Leu Glu His Tyr Leu Gly Leu
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<210> 8

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 8

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Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
35                40                45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
50                55                60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
65                70                75                80

Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys
85                90                95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
100               105               110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
115               120               125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly

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130	135	140	
Thr Ala Ile His Thr	Ala Gln Gly Ile	Ala Ala Ala Arg Lys Glu Ala	
145	150	155	160
Gly Met Asp Ala Gln	Pro Asp Ala Thr	Glu Gln Ala Leu Glu Gly Ser	
	165	170	175
Arg Gly Ala Ser Val Asp	Gly Ile Pro Val His	Ala Val Arg Met Ser	
	180	185	190
Gly Met Val Ala His	Glu Gln Val Ile Phe	Gly Thr Gln Gly Gln Thr	
	195	200	205
Leu Thr Ile Lys Gln Asp	Ser Tyr Asp Arg Asn	Ser Phe Ala Pro Gly	
	210	215	220
Val Leu Val Gly Val	Arg Asn Ile Ala Gln His	Pro Gly Leu Val Val	
	225	230	235
Gly Leu Glu His Tyr	Leu Gly Leu		
	245		
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Met His Phe Gly Lys	Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu		
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gat tac aag aac atg acc aac atc	cgc gta gct atc gta ggc tac gga		96
Asp Tyr Lys Asn Met Thr Asn Ile	Arg Val Ala Ile Val Gly Tyr Gly		
	20	25	30
aac ctg gga cgc agc gtc gaa aag ctt att gcc aag cag	ccc gac atg		144
Asn Leu Gly Arg Ser Val Glu Lys	Leu Ile Ala Lys Gln Pro Asp Met		
	35	40	45
gac ctt gta gga atc ttc tcg	cgc cgg gcc acc ctc gac aca aag acg		192

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr	
50 55 60	
cca gtc ttt gat gtc gcc gac gtg gac aag gcc gac gac gtg gac	240
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp	
65 70 75 80	
gtg ctg ttc ctg tgc atg ggc tcc gcc acc gac atc cct gag gac gca	288
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala	
85 90 95	
cca aag ttc gcg cag ttc gcc tgc acc gta gac acc tac gac aac cac	336
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His	
100 105 110	
cgc gac atc cca cgc cac cgc cag gtc atg aac gaa gcc gcc acc gca	384
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala	
115 120 125	
gcc gcc aac gtt gca ctg gtc tct acc gcc tgg gat cca gga atg ttc	432
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe	
130 135 140	
tcc atc aac cgc gtc tac gca gcg gca gtc tta gcc gag cac cag cag	480
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln	
145 150 155 160	
cac acc ttc tgg ggc cca ggt ttg tca cag gcc cac tcc gat gct ttg	528
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu	
165 170 175	
cga cgc atc cct ggc gtt caa aag gcc gtc cag tac acc ctc cca tcc	576
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser	
180 185 190	
gaa gaa gcc ctg gaa aag gcc cgc cgt gcc gaa gcc gcc gac ctc acc	624
Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr	
195 200 205	
gga aag caa acc cac aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc	672
Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala	
210 215 220	
gac cac gag cgc atc gaa aac gac atc cgc acc atg cct gat tac ttc	720
Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe	
225 230 235 240	
gtt gcc tac gaa gtc gaa gtc aac ttc atc gac gaa gca acc ttg gac	768
Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp	
245 250 255	
gcc gag cac acc gcc atg cca cac gcc gga cac gtg atc acc acc gcc	816
Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly	
260 265 270	
gac acc ggt gcc ttc aac cac acc gtg gaa tac atc ctg aag ctg gac	864
Asp Thr Gly Thr Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp	
275 280 285	
cga aac cca gat ttc acc gct tct tca cag atc gct ttc gcc cgc gca	912
Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala	
290 295 300	

gct cac cgc atg aag cag cag ggc caa agc ggt gct ttc acc gtc ctc 960  
Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu 320  
305 310 315

gaa gtt gct cca tac ttg ctc tcc ccg gag aac ttg gat gat ctg atc 1008  
Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile 335  
325 330

gca cgc gac gtc taa 1023  
Ala Arg Asp Val  
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<213> Corynebacterium glutamicum

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Met His Phe Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu  
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20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
145 150 155 160



His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
180 185 190

Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp  
245 250 255

Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly  
260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp  
275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala  
290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu  
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Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile  
325 330 335

Ala Arg Asp Val  
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<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg      96
Arg Asn Ala Val Arg Gln Asp Glu Gly Val Val Thr Val Ala Gly Val
20 25 30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc      144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc      192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

ggt gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag      240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg      288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc      336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg      384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa      432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac      480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

gtg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc      528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc      576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

ggt tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg      624
Gly Ser Ala Phe Glu Ala Ala Lys Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc      672
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

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atc cac-agg gaa cta ggt gtc-gcc-ctt-cct. gag. ctg gac ctc ggt ggc Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly 245 250 255	768
gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala 260 265 270	816
gaa gtc gcc tcc gac cta ctc acc gca gtc gga aaa atg gca gcg gaa Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu 275 280 285	864
cta ggc atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile 290 295 300	912
gca ggc ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa aac Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn 305 310 315 320	960
gtc cac gta gac gac gac aaa acc cgc cgc tac gta gcc gtc gac gga Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly 325 330 335	1008
ggc atg tcc gac aac atc cgc cca gca ctc tac ggc tcc gaa tac gac Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp 340 345 350	1056
gcc cgc gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg 355 360 365	1104
atc gtg ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu 370 375 380	1152
atc tac cca tct gac atc acc agc ggc gac ttc ctc gca ctc gca gcc Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala 385 390 395 400	1200
acc ggc gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr 405 410 415	1248
cgg ccc gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu 420 425 430	1296
cgc cgc gaa acc ctc gac gac atc ctc tca cta gag gca taa Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala 435 440 445	1338

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<212> PRT

<213> Corynebacterium glutamicum

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20 25 30  
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val  
35 40 45  
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe  
50 55 60  
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys  
65 70 75 80  
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala  
85 90 95  
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser  
100 105 110  
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala  
115 120 125  
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu  
130 135 140  
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp  
145 150 155 160  
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe  
165 170 175  
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser  
180 185 190  
Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu  
195 200 205  
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala  
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln  
 225 230 235 240  
 Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly  
 245 250 255  
 Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala  
 260 265 270  
 Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu  
 275 280 285  
 Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile  
 290 295 300  
 Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn  
 305 310 315 320  
 Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly  
 325 330 335  
 Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp  
 340 345 350  
 Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg  
 355 360 365  
 Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu  
 370 375 380  
 Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala  
 385 390 395  
 Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr  
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 Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala  
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<213> Corynebacterium glutamicum

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1      5      10

cgc aat gcc gtg cgc caa gaa gac gcc gtt gtc acc gtc gct ggt gtg      96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20     25     30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc      144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35     40     45

gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc      192
Asp Glu Pro Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50     55     60

ggt gga cca gcc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag      240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65     70     75     80

acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca      288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85     90     95

tcc atc aac gaa ctg gcc att gcc ctg gcc gct ggt ttc ccc gcc agc      336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100    105    110

cgt atc acc gcg cac gcc aac aac aaa gcc gta gag ttc ctg cgc gcg      384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115    120    125

ttg gtt caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa      432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130    135    140

cta gaa ctg ttg gat tac gtt gcc gct ggt gaa gcc aag att cag gac      480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145    150    155    160

gtg ttg atc cgc gta aag cca gcc atc gaa gca cac acc cac gag ttc      528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165    170    175

atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc      576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180    185    190

ggt tcc gca ttc gaa gca gca aaa gcc gcc aac gca gaa aac ctg      624

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Gly	Ser	Ala	Phe	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Asn	Ala	Glu	Asn	Leu		
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aac	ctg	gtt	ggc	ctg	cac	tgc	cac	gtt	ggc	tcc	cag	gtg	ttc	gac	gcc	672	
Asn	Leu	Val	Gly	Leu	His	Cys	His	Val	Gly	Ser	Gln	Val	Phe	Asp	Ala		
	210					215					220						
gaa	ggc	ttc	aag	ctg	gca	gca	gaa	cgc	gtg	ttg	ggc	ctg	tac	tca	cag	720	
Glu	Gly	Phe	Lys	Leu	Ala	Ala	Glu	Arg	Val	Leu	Gly	Leu	Tyr	Ser	Gln		
225					230					235				240			
atc	cac	agc	gaa	ctg	ggc	gtt	gcc	ctt	cct	gaa	ctg	gat	ctc	ggc	ggc	768	
Ile	His	Ser	Glu	Leu	Gly	Val	Ala	Leu	Pro	Glu	Leu	Asp	Leu	Gly	Gly		
			245						250					255			
gga	tac	ggc	att	gcc	tat	acc	gca	gct	gaa	gaa	cca	ctc	aac	gtc	gca	816	
Gly	Tyr	Gly	Ile	Ala	Tyr	Thr	Ala	Ala	Glu	Glu	Pro	Leu	Asn	Val	Ala		
			260						265					270			
gaa	gtt	gcc	tcc	gac	ctg	ctc	acc	gca	gtc	gga	aaa	atg	gca	gcg	gaa	864	
Glu	Val	Ala	Ser	Asp	Leu	Leu	Thr	Ala	Val	Gly	Lys	Met	Ala	Ala	Glu		
	275						280					285					
cta	ggc	atc	gac	gca	cca	acc	gtg	ctt	gtt	gag	ccc	ggc	cgc	gct	atc	912	
Leu	Gly	Ile	Asp	Ala	Pro	Thr	Val	Leu	Val	Glu	Pro	Gly	Arg	Ala	Ile		
	290					295					300						
gca	ggc	ccc	tcc	acc	gtg	acc	atc	tac	gaa	gtc	ggc	acc	acc	aaa	gac	960	
Ala	Gly	Pro	Ser	Thr	Val	Thr	Ile	Tyr	Glu	Val	Gly	Thr	Thr	Lys	Asp		
305					310				315					320			
gtc	cac	gta	gac	gac	gac	aaa	acc	cgc	cgt	tac	atc	gcc	gtg	gac	gga	1008	
Val	His	Val	Asp	Asp	Asp	Lys	Thr	Arg	Arg	Tyr	Ile	Ala	Val	Asp	Gly		
				325					330					335			
ggc	atg	tcc	gac	aac	atc	cgc	cca	gca	ctc	tac	ggc	tcc	gaa	tac	gac	1056	
Gly	Met	Ser	Asp	Asn	Ile	Arg	Pro	Ala	Leu	Tyr	Gly	Ser	Glu	Tyr	Asp		
			340				345						350				
gcc	cgc	gta	gta	tcc	cgc	ttc	gcc	gaa	gga	gac	cca	gta	agc	acc	cgc	1104	
Ala	Arg	Val	Val	Ser	Arg	Phe	Ala	Glu	Gly	Asp	Pro	Val	Ser	Thr	Arg		
		355				360						365					
atc	gtg	ggc	tcc	cac	tgc	gaa	tcc	ggc	gat	atc	ctg	atc	aac	gat	gaa	1152	
Ile	Val	Gly	Ser	His	Cys	Glu	Ser	Gly	Asp	Ile	Leu	Ile	Asn	Asp	Glu		
	370					375					380						
atc	tac	cca	tct	gac	atc	acc	agc	ggc	gac	ttc	ctt	gca	ctc	gca	gcc	1200	
Ile	Tyr	Pro	Ser	Asp	Ile	Thr	Ser	Gly	Asp	Phe	Leu	Ala	Leu	Ala	Ala		
385					390					395				400			
acc	ggc	gca	tac	tgc	tac	gcc	atg	agc	tcc	cgc	tac	aac	gcc	ttc	aca	1248	
Thr	Gly	Ala	Tyr	Cys	Tyr	Ala	Met	Ser	Ser	Arg	Tyr	Asn	Ala	Phe	Thr		
			405						410					415			
cgg	ccc	gcc	gtc	gtg	tcc	gtc	cgc	gct	ggc	agc	tcc	cgc	ctc	atg	ctg	1296	
Arg	Pro	Ala	Val	Val	Ser	Val	Arg	Ala	Gly	Ser	Ser	Arg	Leu	Met	Leu		
			420				425						430				
cgc	cgc	gaa	acg	ctc	gac	gac	atc	ctc	tca	cta	gag	gca	taa			1338	
Arg	Arg	Glu	Thr	Leu	Asp	Asp	Ile	Leu	Ser	Leu	Glu	Ala					
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<212> PRT

<213> *Corynebacterium glutamicum*

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20 25 30  
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35 40 45  
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe  
50 55 60  
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys  
65 70 75 80  
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala  
85 90 95  
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser  
100 105 110  
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala  
115 120 125  
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu  
130 135 140  
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp  
145 150 155 160  
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe  
165 170 175  
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser  
180 185 190  
Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu



195	200	205
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala 210 215 220		
Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln 225 230 235 240		
Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly 245 250 255		
Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala 260 265 270		
Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu 275 280 285		
Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile 290 295 300		
Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp 305 310 315 320		
Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly 325 330 335		
Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp 340 345 350		
Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg 355 360 365		
Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu 370 375 380		
Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala 385 390 395 400		
Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr 405 410 415		
Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu 420 425 430		
Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala 435 440 445		

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(753)

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1 5 10 15

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg 96  
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat 144  
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc 192  
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg 240  
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac 288  
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

gcg cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga 336  
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

gaa tcg gaa gta gtg gtg ccc act ctc atc gat gaa gat ccg cag ttg 384  
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
115 120 125

cgt gaa ctt ttc atg cac gcc atg gat gag tct cgg ttc gct ttc aat 432  
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
130 135 140

gag ctg ctt aat gcg ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca 480  
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
145 150 155 160

ctt tta agg aaa aag cag gct cgt caa gca gct cgc gct gtg ctg ccc 528  
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
165 170 175

aac gct aca gag tcc aga atc gtg gtg tct gga aac ttc cgc acc tgg 576  
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
180 185 190

agg cat ttc att ggc atg cga gcc agt gaa cat gca gac gtc gaa atc 624  
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
195 200 205

cgc gaa gta gcg gta gga tgt tta aga aag ctg cag gta gca gcg cca 672  
Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
210 215 220

act gtt ttc ggt gat ttt gag att gaa act ttg gca gac gga tcg caa 720  
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
225 230 235 240

atg gca aca agc ccg tat gtc atg gac ttt taa 753  
Met Ala Thr Ser Pro Tyr Val Met Asp Phe  
245 250

<210> 16

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu

115	120	125	
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn 130 135 140			
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala 145 150 155 160			
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro 165 170 175			
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp 180 185 190			
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile 195 200 205			
Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro 210 215 220			
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln 225 230 235 240			
Met Ala Thr Ser Pro Tyr Val Met Asp Phe 245 250			
<210> 17			
<211> 551			
<212> DNA			
<213> Corynebacterium glutamicum			
<400> 17			
aaccggtgtg gagccgacca ttccgcgagg ctgcactgca acgaggtcgt agtttttgta	60		
catggcttct ggccagttca tggattggct gccgaagaag ctataggcat cgccaccagg	120		
gccaccggag ttaccgaaga tgggtgccgtg cttttcgcct tgggcaggga ccttgacaaa	180		
gcccacgctg atatcgccaa gtgagggtac agaatagtgc atgggcacgt cgatgctgcc	240		
acattgagcg gaggcaatat ctacctgagg tgggcattct tccagcggga tgttttcttg	300		
cgctgctgca gtgggcattg atacaaaaa ggggctaagc cgagtcgagg cggcaagaac	360		
tgctaactacc ttttttattg tcgaacgggg cattacggct ccaaggacgt ttgtttctg	420		
ggtcagttac cccaaaaagc atatacagag accaatgatt ttctattaaa aaggcaggga	480		
tttgttataa gtatgggtcg tattctgtgc gacgggtgta cctcggctag aatttctccc	540		

catgacacca g

551

<210> 18

<211> 365

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(365)

<400> 18

gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct 48  
Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
1 5 10 15

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg 96  
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat 144  
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc 192  
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg 240  
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac 288  
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga 336  
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

gaa tcg gaa gta gtg gtg ccc act ctc at 365  
Glu Ser Glu Val Val Val Pro Thr Leu Ile  
115 120

<210> 19

<211> 122

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 19

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile  
115 120

<210> 20

<211> 833

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(833)

<400> 20  
atg gct aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca 48  
Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro  
1 5 10 15

cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg 96  
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val  
20 25 30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val	144
35 40	
gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe	192
50 55 60	
ggg gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys	240
65 70 75 80	
acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala	288
85 90 95	
tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser	336
100 105 110	
cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala	384
115 120 125	
ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu	432
130 135 140	
ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp	480
145 150 155 160	
gtg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe	528
165 170 175	
atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc Ile Ala Thr Ser Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser	576
180 185 190	
ggg tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu	624
195 200 205	
aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala	672
210 215 220	
gaa ggc ttc aag ctg gca gca gag cgc gtg ttg ggc ctg tac tca cag Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln	720
225 230 235 240	
atc cac agc gaa cta ggt gtc gcc ctt cct gag ctg gac ctc ggt ggc Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly	768
245 250 255	
gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala	816
260 265 270	
gaa gtc gcc tcc gac ct Glu Val Ala Ser Asp Leu	833
275	

<210> 21

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 21

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro  
1 5 10 15

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val  
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val  
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe  
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys  
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala  
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser  
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala  
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu  
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp  
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe  
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser  
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu  
195 200 205



Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala  
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln  
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly  
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala  
260 265 270

Glu Val Ala Ser Asp Leu  
275

<210> 22

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 22  
gggtacctcg cgaagtagca cctgtcac 28

<210> 23

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 23  
gcggatcccc catcgcccct caaaga 26

<210> 24

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 24

aacggg<sup>g</sup>cgg<sup>t</sup> gaagg<sup>g</sup>caac t

21

<210> 25

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 25

tga<sup>a</sup>agacag g<sup>g</sup>t<sup>t</sup>atccag a

21

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 26

ccatggtacc aag<sup>t</sup>gcgtg<sup>g</sup> cgag

24

<210> 27

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 27

ccatgggtacc acactgtttc ctgtgc 25

<210> 28

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 28  
ctggttccgg cgagtggagc cgaccattcc gcgagg 36

<210> 29

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 29  
ctcgctccgg cgaggtcgga ggcaacttct gcgacg 36

<210> 30

<211> 6

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 30  
ggtacc 6

<210> 31

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 31  
ggatcttcac ctagatcc

18

<210> 32

<211> 16

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 32  
ccctgataaa tgcttc

16

<210> 33

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 33  
ccggagaaga tgtaacaatg gctac

25

<210> 34

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 34

cctcgactgc agacccttag acacc

25

<210> 35

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 35

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30

Gly Asn Asp Val Val Val Val Val Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
 405 410 415

Ala Gly Thr Gly Arg  
 420

<210> 36

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg  
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Asp Lys Val Ser Leu Val Gly Ala  
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
405 410 415

Ala Gly Thr Gly Arg  
420

<210> 37

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 37



Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
 1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
 20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Val Gly  
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg  
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
405 410 415

Ala Gly Thr Gly Arg  
420